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#7

RAW SEQUENCE LISTING

DATE: 03/03/2003

PATENT APPLICATION: US/09/832,189A

TIME: 12:54:19

Input Set : A:\PH-1167US seq-revised.txt

Output Set: N:\CRF4\03032003\I832189A.raw

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3 <110> APPLICANT: RIKEN
5 <120> TITLE OF INVENTION: Truncated Reelin Protein and DNA Encoding the Same
7 <130> FILE REFERENCE: PH-1167
9 <140> CURRENT APPLICATION NUMBER: US 09/832,189A
10 <141> CURRENT FILING DATE: 2001-04-11
12 <150> PRIOR APPLICATION NUMBER: JP 2000-109954
13 <151> PRIOR FILING DATE: 2000-04-11
15 <160> NUMBER OF SEQ ID NOS: 28
17 <170> SOFTWARE: PatentIn Ver. 2.0
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20 <211> LENGTH: 2274
21 <212> TYPE: DNA
22 <213> ORGANISM: Xenopus laevis
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25 <221> NAME/KEY: misc_feature
26 <222> LOCATION: (100)
27 <223> OTHER INFORMATION: a or g or t or c
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (157)..(1455)
33 <220> FEATURE:
34 <221> NAME/KEY: sig_peptide
35 <222> LOCATION: (157)..(234)
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: (241)..(726)
40 <223> OTHER INFORMATION: F-spondin domain
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (847)..(1197)
45 <223> OTHER INFORMATION: CR-50 epitope region
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W--> 50 aaccattaat tatatatatta tataaatata tatatataaan ctctgtatcc caggctgctt 120
52 atgaagaaaag ctcatthaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174
53                                     Met Glu Leu Leu His Thr
54                                     1           5
56 ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222
57 Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys
58      10           15           20
60 ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270
61 Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe
62      25           30           35

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64 ttt ttc ctt tgc act cat cat gga gaa ctg gaa gga gat ggg gaa caa 318
65 Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu Gln
66      40      45      50
68 gga gaa gtg ctc atc tct ctg cac ctg gcg ggc aac ccc agc tac tac 366
69 Gly Glu Val Leu Ile Ser Leu His Leu Ala Gly Asn Pro Ser Tyr Tyr
70 55      60      65      70
72 ata cct ggg cag gag tac cat gtg acc ata tcc act agt acc ttc ttt 414
73 Ile Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe Phe
74      75      80      85
76 gat ggt ctt ctg gtg act gga ctt tac act tct acc agt gtt caa gcg 462
77 Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Val Gln Ala
78      90      95      100
80 tct cag agc att gga ggc tct aaa gca ttt gga ttt ggt att atg agc 510
81 Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe Gly Phe Gly Ile Met Ser
82      105      110      115
84 gac cgt cag ttt ggt acc cag ttt atg tgc agt gtc gtt gct tcc cac 558
85 Asp Arg Gln Phe Gly Thr Gln Phe Met Cys Ser Val Val Ala Ser His
86      120      125      130
88 gtg agt cat ctt ccc aca aca aac cta agt ttt gta tgg att gca cca 606
89 Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe Val Trp Ile Ala Pro
90 135      140      145      150
92 cca gca ggt aca gga tgt gtc aac ttc atg gcc aca gca aca cat agg 654
93 Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His Arg
94      155      160      165
96 gga caa gtt att ttc aag gat gcc ctg gca caa caa ctg tgc gaa caa 702
97 Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu Gln
98      170      175      180
100 gga gct cct act gaa gct ccc ttg cgg cct aat tta gcc gaa att cac 750
101 Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro Asn Leu Ala Glu Ile His
102      185      190      195
104 agt gaa agc atc ctt tta cga gat gat ttt gac tca tat aag ctt cag 798
105 Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe Asp Ser Tyr Lys Leu Gln
106      200      205      210
108 gaa ttg aat cca aat att tgg ctc cag tgc aga aat tgc gaa gtt ggt 846
109 Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys Arg Asn Cys Glu Val Gly
110 215      220      225      230
112 gag cag tgt ggt gca att atg cat ggt ggg gca gtc act ttt tgt gat 894
113 Glu Gln Cys Gly Ala Ile Met His Gly Gly Ala Val Thr Phe Cys Asp
114      235      240      245
116 ccg tat gga cca aga gaa ttg ata act gtt caa atg aac aca act acg 942
117 Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val Gln Met Asn Thr Thr Thr
118      250      255      260
120 gca tct gtt ttg cag ttt tct att ggg tca gga tgc tgc agg ttc agc 990
121 Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe Ser
122      265      270      275
124 tat tca gac cct gga att gtg gtg tca tac aca aag aat aat tca tct 1038
125 Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr Thr Lys Asn Asn Ser Ser
126      280      285      290
128 agt tgg atg cca ttg gag aga att agt gct cct tcc aat gtt agc acc 1086

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129 Ser Trp Met Pro Leu Glu Arg Ile Ser Ala Pro Ser Asn Val Ser Thr
130 295 300 305 310
132 atc att cac att att tac cta cct cct gaa gct aaa gga gaa aat gtg 1134
133 Ile Ile His Ile Ile Tyr Leu Pro Pro Glu Ala Lys Gly Glu Asn Val
134 315 320 325
136 aaa ttc cgt tgg agg cag gag aac atg cag gca ggt gat gtg tat gaa 1182
137 Lys Phe Arg Trp Arg Gln Glu Asn Met Gln Ala Gly Asp Val Tyr Glu
138 330 335 340
140 gcc tgc tgg gca ctg gat aac att ttg att atc aat gct gct cat aaa 1230
141 Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile Ile Asn Ala Ala His Lys
142 345 350 355
144 gaa gtc gtg tta gaa gac aat cta gat cca atg gac aca gga aac tgg 1278
145 Glu Val Val Leu Glu Asp Asn Leu Asp Pro Met Asp Thr Gly Asn Trp
146 360 365 370
148 ctt ttt ttc cct ggg gct act gta aag cat acc tgt cag tcg gat gga 1326
149 Leu Phe Phe Pro Gly Ala Thr Val Lys His Thr Cys Gln Ser Asp Gly
150 375 380 385 390
152 aac tct ata tat ttt cat ggt aca gaa agc agt gaa tac aac ttt gct 1374
153 Asn Ser Ile Tyr Phe His Gly Thr Glu Ser Ser Glu Tyr Asn Phe Ala
154 395 400 405
156 act acc aga gat gtg gat ctt tcc agt gag gac atc cag gac cag tgg 1422
157 Thr Thr Arg Asp Val Asp Leu Ser Ser Glu Asp Ile Gln Asp Gln Trp
158 410 415 420
160 tct gaa gag ttt gag aat cta cca gct ggg taa atttttagatg tagccatgag 1475
161 Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly
162 425 430
164 cattacattt tatcacgtga aaatgcaaga aacagtattt atatacatat tttaaagggtc 1535
166 aatacagaac cctataaatg gcagggttagg gctaccatgt aaatattttt aatgttcata 1595
168 atgtcatagg tggtaagtat ttacatagc agttactgat tgattattat tgtttgtctt 1655
170 ttacccagtt acagctaaca cacaggcat ttttttccaa tggcaacatc cattttgccg 1715
172 ctctgagcag aacatttggt tcatattatg catttgaacc tgtgtctatg agagtgcagc 1775
174 taaaataaac ttcttggtta tgggtgttac catacaaacac tggtagctca tgacatatga 1835
176 aaaatatgac tcacattaaa tcagtaagat cagttcaagt atagtacggt gcattaatct 1895
178 gccaataaac atttagaatt gtattttata ttttatattt aagattagaa ttgactccat 1955
180 tcttgtagct tgcatcacat ttgtggctag tttatgggtc aatagacagc catcatacat 2015
182 tagtcagagt aaatcgagca ttacaaaact caatgagcca tagtgagtgt gacaatcaga 2075
184 agtgactgtc aagtaaataca accatttgct catacagatg cacatttgaa cagtggattc 2135
186 ttatccagaa agggccattt ttactatca ctctgggatt taaatgccac ttctaattgg 2195
188 aacttccagg tcacaaaaat agaatggaca tttaaacatc atggtttctca ttacccttaa 2255
190 taaaactccg gttttttta 2274
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194 <211> LENGTH: 432
195 <212> TYPE: PRT
196 <213> ORGANISM: Xenopus laevis
198 <400> SEQUENCE: 2
199 Met Glu Leu Leu His Thr Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu
200 1 5 10 15
202 Phe Thr Gly Ile Leu Cys Phe Val Val Ala Arg Gly Val Gly Tyr Tyr
203 20 25 30

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205 Pro Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu
206          35          40          45
208 Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala
209          50          55          60
211 Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile
212 65          70          75          80
214 Ser Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr
215          85          90          95
217 Ser Thr Ser Val Gln Ala Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe
218          100          105          110
220 Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys
221          115          120          125
223 Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser
224          130          135          140
226 Phe Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met
227 145          150          155          160
229 Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala
230          165          170          175
232 Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro
233          180          185          190
235 Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe
236          195          200          205
238 Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys
239          210          215          220
241 Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly
242 225          230          235          240
244 Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val
245          245          250          255
247 Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser
248          260          265          270
250 Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr
251          275          280          285
253 Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala
254          290          295          300
256 Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu
257 305          310          315          320
259 Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln
260          325          330          335
262 Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile
263          340          345          350
265 Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro
266          355          360          365
268 Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His
269          370          375          380
271 Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser
272 385          390          395          400
274 Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu
275          405          410          415
277 Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly

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Output Set: N:\CRF4\03032003\I832189A.raw

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278          420          425          430
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282 <211> LENGTH: 2745
283 <212> TYPE: DNA
284 <213> ORGANISM: Mus musculus
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287 <221> NAME/KEY: CDS
288 <222> LOCATION: (283)..(2052)
290 <220> FEATURE:
291 <221> NAME/KEY: sig_peptide
292 <222> LOCATION: (283)..(363)
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (284)..(849)
297 <223> OTHER INFORMATION: F-spondin domain
299 <220> FEATURE:
300 <221> NAME/KEY: misc_feature
301 <222> LOCATION: (970)..(1320)
302 <223> OTHER INFORMATION: CR-50 epitope region
304 <400> SEQUENCE: 3
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307 cccgcggccc cggttccccc cgcgctctcg ctccggcggc ccaaagtaac ttcggggagcc 120
309 tcggtctccc gtaacttcc ccccgcgggc tcggttgccc ggaccgctc ggctcgagcc 180
311 cgccgcggc tcgcttccc cgcacgcggc tctccgtgc cggtgctcc gaaagtggat 240
313 gagagagcgc gcggggcgcg cggcggcacg gagcgggcg gc atg gag cgc ggc 294
314                                     Met Glu Arg Gly
315                                     1
317 tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342
318 Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala
319   5          10          15          20
321 acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390
322 Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro
323          25          30          35
325 ttc ttt ttc ctg tgc acc cac cac ggg gag ctg gaa ggg gat ggg gag 438
326 Phe. Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu
327          40          45          50
329 cag ggc gag gtg ctc att tcc ctg cac att gcg ggc aac ccc acc tac 486
330 Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly Asn Pro Thr Tyr
331          55          60          65
333 tac gta ccg gga cag gaa tac cat gtt aca att tca aca agc acc ttc 534
334 Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe
335          70          75          80
337 ttt gat ggc ttg ctg gtg acg gga ctc tat acc tcg aca agc atc cag 582
338 Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Ile Gln
339 85          90          95          100
341 tct tct cag agc att gga ggc tcc agc gcc ttt gga ttc ggg atc atg 630
342 Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly Phe Gly Ile Met
343          105          110          115
345 tcc gac cac cag ttt ggt aac cag ttt atg tgc agt gtg gtg gcc tct 678

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\PH-1167US seq-revised.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 100
Seq#:5; N Pos. 8

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1

VERIFICATION SUMMARY

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Input Set : A:\PH-1167US seq-revised.txt

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L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:60

L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0